

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 5, 2002, 13:47:39 ; Search time 3997.53 seconds
(without alignments)
13376.994 Million cell updates/sec

Title: US-08-153-397A-1
Sequence: 3962
1 CGGGCCTGAGACTGGGTGA.....AAAAAAAAACCGGATTC 3962

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: EST:*

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1720	43.4	2633	11	BC006836 Mus muscu
2	960	24.2	1010	9	AL539517 AL539517
3	815.2	20.6	1019	9	AL528663 AL528663
4	814.6	20.6	987	9	AL528664 AL528664
5	761.6	19.2	898	10	BM043544 BM043544
6	715.8	18.1	770	10	BT257820 BT257820
7	715	18.0	948	10	B1825684 B1825684
8	684	17.3	799	10	B6912321 B6912321
9	680.4	17.2	715	10	BE744806 BE744806
10	672.4	17.0	744	10	BF345815 BF345815
11	672	17.0	744	10	B1193181 B1193181
12	662.6	16.7	772	9	BG696171 BG696171
13	660.2	16.7	772	9	AL043251 AL043251
14	655.6	16.5	912	10	BE304984 BE304984
15	654.6	16.5	662	10	BF944646 BF944646
16	653.8	16.5	877	10	BE249888 BE249888
17	652	16.5	957	10	BE737252 BE737252

18	651.4	16.4	653	10	B1554126 B1554126
19	650.8	16.4	683	10	BG752521 BG752521
20	650.4	16.4	685	10	BG403848 BG403848
21	646.4	16.3	787	10	BF338761 BF338761
22	646	16.3	1144	10	BF527983 BF527983
23	644.2	16.3	684	10	BM046697 BM046697
24	643.6	16.2	898	10	BE898332 BE898332
25	640.8	16.2	801	10	BE735635 BE735635
26	639.6	16.1	1018	10	BE899403 BE899403
27	636.2	16.1	759	10	BF344637 BF344637
28	635	16.0	921	10	BF792714 BF792714
29	632.2	16.0	1009	10	BE613181 BE613181
30	631.2	15.9	759	10	BC913935 BC913935
31	629.2	15.9	711	10	BC541910 BC541910
32	628.4	15.9	1150	10	BF344537 BF344537
33	627.4	15.8	652	9	AL047539 AL047539
34	627.2	15.8	804	10	BC696424 BC696424
35	626.6	15.8	977	10	BC386352 BC386352
36	624	15.7	732	10	BF339561 BF339561
37	622	15.7	676	10	B1772015 B1772015
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39	620.8	15.7	626	9	AM376875 AM376875
40	619.6	15.6	1037	10	BF529368 BF529368
41	618.2	15.6	701	10	B1822991 B1822991
42	613	15.5	680	10	BC818241 BC818241
43	603.6	15.2	649	10	BE304585 BE304585
44	602.4	15.2	1325	10	BF966734 BF966734
45	601	15.2	812	10	B1458024 B1458024

ALIGNMENTS

RESULT 1

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

COMMENT

BC006836 2633 bp. mRNA linear. HNC 12-JUL-2001
Mus musculus, similar to discoidin domain receptor family, member
1, clone IMAGE:358142, mRNA.
BC006836
BC006836.1 GI:14711754
HNC.
house mouse.
Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Submitted (27-APR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
Contact: MGC help desk
Email: cgabs-remail@ncl.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: villalob@bcm.tmc.edu
Villalob, D.K., Luna, R.A., Hale, S.M., Huylk, S., Lu, X., Garcia,
A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,
Muzny, D.M., Gibbs, R.A.,
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>
Series: IRRA Plate: 16 Row: 0 Column: 14
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis

QY	2194	ACCTGTTGTAGTGCAGACAGCCCTCAAGATCTGTCAGTCTGTATTTCCCTTAATGTGC	2253
Db	1818	ACCTGTGTAGTAGTAGAGACCCGCAAGATCTGGTCAAGTGAAGTACTTCCCTATCAGTGTGC	1877
QY	2254	GTAAGGACACACCTTTGGTGTAGTGTCAAGTATCTTACGGCCAGATGGCCACCAAAATG	2313
Db	1878	ACAAGGACACACCCCTTGTGCTGTAGCAGTGAAGTCTCTCCGGCCAGATGCCACCAAAATG	1937
QY	2314	CCAGCTTCTCTTGTCTCCAGGAATGATTTCTCTGAAAGAGTGAAGATCANGTCGAGCG	2373
Db	1938	-----CCAGGAATGATTTCTCTGAAAGAGTGAAGATCANGTCGAGCG	1979
QY	2374	TCGAAGACCCCAACATCATTTGGGCTGCTGGGGGTGTGTGTGACAGACACCCCTCTGCA	2433
Db	1980	TGAAGACCCCAACATCATTCGGTCTCTGGGTGTGTGTGTGTGACAGTACACCCCTCTGCA	2039
QY	2434	TGATTAAGTACTACATGAGAGAACGGGACCTCAACAGTATCTCCATGTGCCACACAGCTGG	2493
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QY	2494	AGGACAGGCAAGCCGAGGGGGCCCTGTGGGAGCGGGCAGGCTGTGCGAGGGGGCCCAACATCA	2553
Db	2100	AGAACAGGCGCACTCAAGGGGCTCTGTGGGAGACAGAGATGTACACAGGGGGCCCAACATCA	2159
QY	2554	GGTACCCATATGATGGTGCATATGTGGACGCCACATGCGCCCTCCGCAATGGCTATCTGCGCA	2613
Db	2160	GCTACCTATATGTGTATCACGTTGGGGGGCCCAATGCGCTCTGTGCAATGCTTATCTGCGCA	2219
QY	2614	CACATCACTTTGTATCATCTGGGACCTGTGGCCAGCGAGACTGCTAGTTGGGGAAATTTCA	2673
Db	2220	CGCTGAAGCTTTGTGATCGGGACCTGTGGCCAGCGAGACTGCTAGTTGGGGAAATTTCA	2279
QY	2674	CCATCAAAATGCGACACTTTGGCATGAGCCGGAACTCTATCTGTGGGACTATTTACCGTG	2733
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QY	2734	TGCAGGGCCGGGACAGTGTGCTGCCATCCGCTGGATGGCCGTGGGAGTGCATCATAGGGGA	2793
Db	2340	TCCAGGGCCGGGCGGTGCTGCCATCAGTGGATGGCTTTGGGAGTGCATCATATGGGGGA	2399
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QY	2914	AGTTCTTCGGGAGACAGGGCCGGCAGGTGTACTCTGCCCGGCGGCGTCCGCCGAGC	2973
Db	2520	AGTTCTTCAGGAGACAGGGCCGGCAGGTGTACTCTGTCCAGGCAACCCGCTTCCACAGCA	2579
QY	2974	GCCATATATGAGCTGATGCTTGTGGTGTCTGTGGAGCCGGGAGTGTGAGCAGCAGACAC	3027
Db	2580	CCCTGTATGAGCTGATGCTCCGGTGTGTGGAGCCGGGAGCCGAGCAGCAGGCGCGC	2633

JOURNAL Unpublished (2001)
 COMMENT Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
 Source 1. 1010
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CSODF03X015"
 /clone_11b="L71.FL013.Fbrn1"
 /dev_stage="pooled tissue from post conception fetuses (20 week, 24 week and 26 week)."
 /lab_host="DH10B"
 /note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville , Maryland 20850, USA Fax : (41) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 191 a 321 c 298 g 199 t 1 others
 ORIGIN

Query Match 24.2% Score 960; DB 9; Length 1010;
 Best Local Similarity 99.5% Pred. No. 1,2e+163;
 Matches 983; Conservative 1; Mismatches 1; Indels 3; Gaps 2;

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 Db 1 AAGCAGCGGAGGGGGCCCCCTGGGAGCGGGAGAGGCTGCGACGAGGGGCCCACTACAGTACC 60
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 QY 2560 CAATCGCTGCTGATGTGGCAGCCCGAGATCGCCTCCGGCATCGCTATGTGGCCACTCA 2619
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 Db 121 ACTTGTCATCAGGGAGCTGGCCAGCGGGAACCTGCTAGTTGGGAAATTTCCACTCA 180
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 QY 2680 AATCGCAGACTTTGGCATGAGCCGGAACCTCTATAGCTGGGGAGCATTAACCGTGCAGG 2739
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 Db 181 AATCGCAGACTTTGGCATGAGCCGGAACCTCTATAGCTGGGGAGCATTAACCGTGCAGG 240
 |||||||
 QY 2740 GCCGGGAGTGTGCCATCCGCTGGATGGGCTGGAGTGCATCCTATGGGGAAGTTCA 2799
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 Db 241 GCCGGGAGTGTGCCATCCGCTGGATGGGCTGGAGTGCATCCTATGGGGAAGTTCA 300
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 QY 2800 GCAGTCCGAGTACGTGTGGGCTTTGGTGTGACCTCTGTGGAGAGTGTGATGCTCTGTA 2859
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 Db 301 GCAGTCCGAGTACGTGTGGGCTTTGGTGTGACCTCTGTGGAGAGTGTGATGCTCTGTA 360
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 Db 361 GGGGCCAGCCCTTTGGGAGGCTCAACCGAGCGAGAGGTCATGAGAGGCGGGAGGAGTCT 420
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 QY 2930 TCCGGGACAGGGCCCGGAGGTTGTAACCTGTCCCGGCGCTGCTGCGCCGAGGGCTAT 2979
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 Db 421 TCCGGGACAGGGCCCGGAGGTTGTAACCTGTCCCGGCGCTGCTGCGCCGAGG -CTAT 478
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 QY 2980 ATGAGCTGATGCTTCGGTGTGTGAGAGCGGGAGTGTGAGCAGCAGCACACCTTTTCCAGC 3039
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 Db 479 ATGAGCTGATGCTTCGGTGTGTGAGAGCGGGAGTGTGAGCAGCAGCACACCTTTTCCAGC 538
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 Db 539 TGCATCGGTTCTCCGAGAGAGATGCATCTCAACAGAGGTGTAAATACACATCCAGCTGCC 598
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 QY 3100 CTCCTCAGGGAGTATCCAGGGGAGGCAAGCAATGACATAAACAAGAGGACACAATGGCA 3159

Db	599	CTCCCTCAGGGAGTGATCCAGGGGAGGACGATGACACTATAAACAAGAGACACATGGCA	658
QY	3160	CCCTCGCCCTTCCTCCCGACAGCCCATACCTTAAATAGAGCGATGAGACTGCAGGT	3219
Db	659	CCTCGCCCTTCCTCCCGACAGCCCATACCTTAAATAGAGCGATGAGACTGCAGGT	718
QY	3220	GGGCGTGGGCCCAACCCAGGAGAGCTGATGGCCCTTCCTCCCTTCGAGACACATGTCATGT	3279
Db	719	GGGCGTGGGCCCAACCCAGGAGAGCTGATGGCCCTTCCTCCCTTCGAGACACATGTCATGT	778
/QY	3280	CCCCCTCTGTTCCTTCCTTAGAAGCCCTGTGCGCCACCCAGCTGATCCTGTGGATG	3339
Db	779	CCCCCTCTGTTCCTTCCTTAGAAGCCCTGTGCGCCACCCAGCTGATCCTGTGGATG	838
QY	3340	GGATCCTTCACACCCTCCTTAGCATATCCCTTGGGGAAGGGGGGAGAAAAATATAGATA	3399
Db	839	GGATCCTTCACACCCTCCTTAGCATATCCCTTGGGGAAGGGGGGAGAAAAATATAGATA	898
QY	3400	GACACTGGACATGGGCCATTGGAGCACCCTGGGCCCACTGGCAACAACATGATTCCTGGAG	3459
Db	899	GACACTGGACATGGGCCATTGGAGCACCCTGGGCCCACTGGCAACAACATGATTCCTGGAG	958
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[illegible]

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/clone="CSDD001YK21"
/clone_11b="LTI_NFL001_NBC4"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact: Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax: (1) 301 610
8311 Email: fliang@lifestech.com URL:
http://fulllength.invitrogen.com"

```

Query Match	20.68;	Score 815.2;	DB 9;	Length 1019;
- Best Local Similarity	89.08;	Pred. No. 1.8e-137;		

Matches 906; Conservative 22; Mismatches 85; Indels 5; Gaps 5;

[illegible]

RESULT 4
AL528664

LOCUS	AL528664		987 bp	mRNA	linear	EST 13-FEB-2001
DEFINITION	AL528664.LTL_NFL001.NBC4 Homo sapiens cDNA clone CS0DD001YK21 5 prime, mRNA sequence.					
ACCESSION	AL528664					
VERSION	AL528664.1		GI:12792157			
KEYWORDS	EST.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
AUTHORS	Li,W.B., Gruber,C., Jesse,J. and Poljans,P.					
TITLE	Full-length cDNA libraries and normalization					
JOURNAL	Unpublished (2001)					
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr. Location/Qualifiers					
FEATURES	source					
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	/db_xref="taxon:9606"					
	/clone="CS0DD001YK21"					
	/clone_id="LTL_NFL001.NBC4"					
	/sex="male"					
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	/lab_host="DH10B"					
	/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a Notti-0119o(47) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"					
BASE COUNT	186 a 263 c 332 g 200 t					6 others
ORIGIN						
Query Match	20.6%; Score 814.6; DB 9; Length 987;					
Best Local Similarity	98.7%; Pred. No. 2,3e-137;					
Matches 848; Conservative	4; Mismatches 3; Indels 4; Gaps 3;					
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Dd	90 AGARTTGTGCCCCCACCCCTTAGGCCCGAGGATCAGAGCTATGGGACCAAGAGCCC					149
Oy	337 TGTGATCTTTACTGCTGCTCTTGAGGCAAGTGGAATGCATCATGAAGGACATT					396
Dd	150 TGTGATCTTTACTGCTGCTCTTGAGGCAAGTGGAATGCATCATGAAGGACATT					209
Oy	397 TTGATCTGCCAAGTCGCGCTATGCCCTGGGACATGACAGACCGAACCATCCAGACAGT					456
Dd	210 TTGATCTGCCAAGTCGCGCTATGCCCTGGGACATGACAGACCGAACCATCCAGACAGT					269
Oy	457 ACATCTCGCTTCAGAGTCCGTGTCGTCATTCACATTCACATTCGCCCCCGCCACACAGAGTTGGAGA					516
Dd	270 ACATCTCGCTTCAGAGTCCGTGTCGTCATTCACATTCACATTCGCCCCCGCCACACAGAGTTGGAGA					329
Oy	517 GCATGACGAGGAGTGGGAGCTGTGTGCCCGCCAGAGGTGGTGTTCACCAAGAGAGAGAGT					576
Dd	330 GCATGACGAGGAGTGGGAGCTGTGTGCCCGCCAGAGGTGGTGTTCACCAAGAGAGAGAGT					387
Oy	577 ACTTGACAGGTGATCTACAACGACTCCACTGTGTGCTGTGTGTGGGACCCAGAGAGAGC					636
Dd	388 ACTTGACAGGTGATCTACAACGACTCCACTGTGTGCTGTGTGTGGGACCCAGAGAGAGC					447
Oy	637 ATGCGGAGGAGCTGGGACAAAGAGATTCCCGGAGATCAACGAGGAGCGCTATCCCGGAGAG					696
Dd	448 ATGCGGAGGAGCTGGGACAAAGAGATTCCCGGAGACTTAACGAGGAGCGCTATCCCGGAGAG					507

0Y 697 GTCGCGCGTGAAGGGGCTGGAAAGACCGCGGGGCTAGAGAGTGATCTACGCCAATGAGG 756
 Db 508 GTCCGCGCTGATGGGCTGGAAAGACCGCGGGGCTAGAGAGTGATCTACGCCAATGAGG 567
 0Y 757 ACCCTGAGGAGAGTGATGCTGAAGGACCTTGAGGCCGCCCATGATGGTGGCCGACTGGTTCCGCT 816
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 0Y 817 TCTACCCCCGGGCTGACCCGGGTCATAGTGTCTGTTCGGGGGTAGAGCTCTATGAGCTGCC 876
 Db 628 TCTACCCCCGGGCTGACCCGGGTCATGAGGCTGTGTGTGGGGGTAGAGCTCTATGAGCTGCC 687
 0Y 877 TCTGAGGAGATGAGACCTCTGTCTTACACCGCCCTGTGGGGGCGAGCAATGATTTATTCG 936
 Db 688 TCTGAGGAGATGAGACCTCTGTCTTACACCGCCCTGT -GGGAGCAATGATTTATTCG 746
 0Y 937 AGCGCGTGTACTCAACGATCCACCTATAGAGGACATACCGTGGGCGAGCTGCAGTATG 996
 Db 747 AGCGCGTGTACTCAACGATCCACCTATAGAGGACATACCGTGGGCGAGCTGCAGTATG 806
 0Y 997 GGGGTCTGGGGCAGCGTGGGAGATGGGTGGTGGGCTGGATGATACCTTAGGAAGAGTCAAG 1056
 Db 807 GGGGTCTGGGGCAGCTGTGCATGGATGGGTGGTGGGCTGGATGATACCTTAGGAAGAGTCAAG 866
 0Y 1057 AGCTCGGGGTCTGGCCAGGCTATGACTATAGTGGATGAGCAACGACACTTCTCCAGTG 1116
 Db 867 AGCTCGGGGTCTGGCCAGGCTATGACTATAGTGGATGAGCAACGACACTTCTCCAGTG 925
 0Y 1117 GCTATGTGAGATGGAGTT 1135
 Db 926 GCTATGTGAGATGGAGTT 944

FEATURES	source
LOCUS	BM043544
DEFINITION	898 bp mRNA
ACCESSION	603619969p1 NIH_MGC_40 Homo sapiens CDNA clone IMAGE:5445617 5',
VERSION	BM043544
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE	1 (bases 1 to 898)
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/ .
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: DCTD/DTF CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLW) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLW at: http://image.llnl.gov Plate: LNCM1926 row: j column: 18 High quality sequence stop: 837. Location/Qualifiers 1. 898 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:5445617" /clone_1bp="NIH_MGC_40" /tissue_type="carcinoma, cell line" /lab_host="DH10B (phage-resistant)" /note="Organ: prostate; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(5). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University

of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH-MGC library."

BASE COUNT 184 a 261 c 274 g 179 t
 ORIGIN

Query Match 19.2%; Score 761.6; DB 10; Length 898;
 Best Local Similarity 96.3%; Pred. No. 8.8e-128;
 Matches 865; Conservative 0; Mismatches 24; Indels 9; Gaps 8;

213 GCCAGCTTCCTCTCTCCAGGAATGATTTCTGAAAGAGGAGATCATGTCCAGG 2372
 2 GCCAGCTTCCTCTCTCCAGGAATGATTTCTGAAAGAGGAGATCATGTCCAGG 61
 2373 CTCAGGACCCCAACATCATTCGGTCTGGGGCTGTGTGACGAGACCCCTCTGC 2432
 62 CTCAGGACCCCAACATCATTCGGTCTGGGGCTGTGTGACGAGACCCCTCTGC 121
 2433 ATGATTAATGATGATGAGAAAGGGGACCTCAACAGTTCTCACTGCCCACACCTG 2492
 122 ATGATTAATGATGATGAGAAAGGGGACCTCAACAGTTCTCACTGCCCACACCTG 181
 2493 GAGAGCAAGGACGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 2552
 182 GAGAGCAAGGACGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 241
 2553 AGCTACCCATGCTGCTGATGAGACCCAGATGCTCCGGGACGCTATCTGCCC 2612
 242 AGCTACCCATGCTGCTGATGAGACCCAGATGCTCCGGGACGCTATCTGCCC 301
 2613 ACATCACTTTGATACATGAGGACCTGGCCACGCGAATGCTAGTTGGGAAATTTTC 2672
 302 ACATCACTTTGATACATGAGGACCTGGCCACGCGAATGCTAGTTGGGAAATTTTC 361
 2673 ACATCACTTTGATACATGAGGACCTGGCCACGCGAATGCTAGTTGGGAAATTTTC 2732
 362 ACATCACTTTGATACATGAGGACCTGGCCACGCGAATGCTAGTTGGGAAATTTTC 421
 2733 GTGAGGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2792
 422 GTGAGGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 481
 2793 AAGTTACGAGCTGAGTGAAGTGTGGGCTTTGGTGTGACCTGTGGAGAGTGTGATG 2852
 482 AAGTTACGAGCTGAGTGAAGTGTGGGCTTTGGTGTGACCTGTGGAGAGTGTGATG 541
 2853 CTCTGTAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2912
 542 CTCTGTAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 601
 2913 GAGTTCTTCGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2972
 602 GAGTTCTTCGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
 2973 GGGCTATAT-GAGCTGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3030
 661 GGGCTATATGAGCTGT 720
 3031 TTTCCAGGCTGATC-GGTTCCGTGGGAG-AGGATGCAATC-AACAGGCTGTGAATACAC 3087
 721 TTTCCAGGCTGATC-GGTTCCGTGGGAG-AGGATGCAATC-AACAGGCTGTGAATACAC 780
 3088 ATCCAGCTGCTCCCTCCCTCAGGAGTGTATCCAGGGG--AAGCAGTATGACTTAAACAAG 3145
 781 ATCAAGTGTGCTCTCTCTCAGGAGTGTATCCAGGGGAGGAGGAGGAGGAGGAGGAG 840
 3146 AGGACACATGAGCACTCTG-CCCTTCCCTCCCGACAGCCCATCACTCTTAATAGAG 3202
 841 AGGACACATGAGCACTCTG-CCCTTCCCTCCCGACAGCCCATCACTCTTAATAGAG 898

RESULT 6

B1257820
 LOCUS B1257820 770 bp mRNA EST 17-JUL-2001
 DEFINITION 602969918F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5109436 5',
 mRNA sequence.
 B1257820
 B1257820.1 GI:14813571
 EST.
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens
 human.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 770)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: Incyte Genomics, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINL at:
 http://image.jnl.gov
 Plate: L14M1265 row: c column: 05
 High quality sequence stop: 765.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_1ib="NIH_MGC_12"
 /tissue_type="cervical carcinoma cell line"
 /note="Organ: cervix; Vector: pCMV-Sport6; Site: 1; NotI;
 Site: 2; SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.4 kb. Library prepared by Life
 Technologies."

FEATURES

source
 1..770
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_1ib="NIH_MGC_12"
 /tissue_type="cervical carcinoma cell line"
 /note="Organ: cervix; Vector: pCMV-Sport6; Site: 1; NotI;
 Site: 2; SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.4 kb. Library prepared by Life
 Technologies."

BASE COUNT 144 a 207 c 262 g 157 t
 ORIGIN

Query Match 18.1%; Score 715.8; DB 10; Length 770;
 Best Local Similarity 97.3%; Pred. No. 1.7e-119;
 Matches 750; Conservative 0; Mismatches 17; Indels 4; Gaps 2;

229 GAAGGTGGCTATCATGAGCGATGGGGTGGACTTGAAGGATGCCAAGATGCTGCC 288
 1 GAAGGTGGCTATCATGAGCGATGGGGTGGACTTGAAGGATGCCAAGATGCTGCC 60
 289 CCCACCCCTTAGCCCGAGGAGATGAGGAGCTATGGGACGAGGCGCTCATCTTAC 348
 61 CCCACCCCTTAGCCCGAGGAGATGAGGAGCTATGGGACGAGGCGCTCATCTTAC 120
 349 TGCTGTGCTCTTGTGGCAAGTGAATGCTGACATGAAGGACATTTTGTATCTGCCA 408
 121 TGCTGTGCTCTTGTGGCAAGTGAATGCTGACATGAAGGACATTTTGTATCTGCCA 180
 409 AGTGGCGCTATGCGCTGGGAGTGCAGAGCGAGCATCCAGACAGTATCTGTCTT 468
 181 AGTGGCGCTATGCGCTGGGAGTGCAGAGCGAGCATCCAGACAGTATCTGTCTT 240
 469 CCAGCTCTGTGATGATTCACATGCGCGCCGACAGCAGAGTGGAGAGCAGTGCAGG 528
 241 CCAGCTCTGTGATGATTCACATGCGCGCCGACAGCAGAGTGGAGAGCAGTGCAGG 300
 529 ATGGGCGCTGTGCGCGCGAGGAGTGTGTTCCCAAGAGAGAGTACTTGCAGGTG 568
 301 ATGGGCGCTGTGCGCGCGAGGAGTGTGTTCCCAAGAGAGAGTACTTGCAGGTG 360
 589 ATCTACAAGCATCCACACTGTGTGCTGTGTGGGACCCAGGAGCGGATGCCGGGGGCC 648
 361 ATCTACAAGCATCCACACTGTGTGCTGTGTGGGACCCAGGAGCGGATGCCGGGGGCC 420

QY 649 TGGGCAAGAGTTCCTCCGGAGCTACCGGCTGCTTACTCCCGGAGTGGCGCGTGA 708
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 Db 421 TGGGCAAGAGTTCCTCCGGAGCTACCGGCTGCTTACTCCCGGAGTGGCGCGTGA 480
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 QY 709 TGGGCTGGAAGACCGGCTGGGGTCAAGAGTGTATCTCAGGCAATGAGACCCGAGAGAG 768
 |||||||
 Db 481 TGGGCTGGAAGACCGGCTGGGGTCAAGAGTGTATCTCAGGCAATGAGACCCGAGAGAG 540
 |||||||
 QY 769 TGGTGTGAAGACCTTGGGCCCCCATATGTTGCCAGTGGTCCCTTACACCCCGGG 828
 |||||||
 Db 541 TGGTGTGAAGACCTTGGGCCCCCATATGTTGCCAGTGGTCCCTTACACCCCGGG 600
 |||||||
 QY 829 CTGACCGGGTCAAG---AGTGTCTGTCTGCGGGTAGAGCTATGGCTCCCTTGAAGGG 885
 |||||||
 Db 601 CTGACCGGGTCAATGAGCACTGTACTGCGGGTAGAAGCTCTATGGCTCCCTTGAAGGG 660
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 QY 886 ATGAGCTCCTGTCTTACACCGGCCCTGTGGGCGAGACAATGTATTTATCTGAGGCGGTG 945
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 Db 661 ATGAGCTCCTGTCTTACACCGGCCCTGTGGGCGAGACAATGTATTTATCTGAGGCGGTG 719
 |||||||
 QY 946 ACCTAAGACATCCACCTTATGACGACATACCTGGGCGGAGCTGACATG 996
 |||||||
 Db 720 ACCTAAGACATCCACCTATGACGACATACCTGGGCGGAGCTGACATG 770
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RESULT 7

LOCUS B1825684 948 bp mRNA linear EST 04-OCT-2001
 DEFINITION 60307266Bp1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5164480 5',
 B1825684
 VERSION B1825684
 KEYWORDS B1825684.1 GI:15937234
 EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NIH-MGC http://mgc.ncl.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: rgs@dsi-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LLM11408 Row: h Column: 17
 High quality sequence stop: 785.

FEATURES

source

1. 948

Location/Qualifiers

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5164480"
 /clone_id="NIH_MGC_119"
 /tissue_type="medulla"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: pCMV-Sport6; Site:1: NciI;
 Site:2: EcoRV (destroyed); RNA source normal medulla from
 anonymous male age 27. Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.3 kb, insert size range
 0.9-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 013. Note:
 this is a NIH-MGC Library."

BASE COUNT

178 a 272 c 296 g 202 t
 ORIGIN

Query Match 18.0%; Score 715; DB 10; Length 948;
 Best Local Similarity 93.0%; Pred. No. 2,3e-119;
 Matches 845; Conservative 0; Mismatches 35; Indels 29; Gaps 8;

QY 2136 CCTCGATCTCGATCCCGCTTCAAGAGAAAGCTTGGCGAGGCCCATGTTGGAGAGTGCAC 2195
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 Db 1 CCTCGATCTCGATCCCGCTTCAAGAGAAAGCTTGGCGAGGCCCATGTTGGAGAGTGCAC 60
 |||||||
 QY 2196 CTGTGTAGAGTGCACAGCCCTCAAGATCTGTGACGCTTGTGATTTCCCTTATGAGGCT 2255
 |||||||
 Db 61 CTGTGTAGAGTGCACAGCCCTCAAGATCTGTGACGCTTGTGATTTCCCTTATGAGGCT 120
 |||||||
 QY 2256 AAGGACACCTTTTGTGTAGCTGTCAAGATCTTACGCGCAGATGCCACCAAGATGCC 2315
 |||||||
 Db 121 AAGGACACCTTTTGTGTAGCTGTCAAGATCTTACGCGCAGATGCCACCAAGATGCC 178
 |||||||
 QY 2316 AGCTTCTCCTTGTCTCCAGGAATGATTTCTGAAAGAGGTGAAGATCATGTGAGGCTC 2375
 |||||||
 Db 179 -----CCAGGAATGATTTCTGAAAGAGGTGAAGATCATGTGAGGCTC 222
 |||||||
 QY 2376 AAGGACCCCAATCATTTAGGCTGTGGGCGGTGTGTGTGTCAGAGAGACCCCTTGCATG 2435
 |||||||
 Db 223 AAGGACCCCAATCATTTAGGCTGTGGGCGGTGTGTGTGTCAGAGAGACCCCTTGCATG 282
 |||||||
 QY 2436 ATTACTAGTACATGAGAGAACGGCGACCTCAACACGATTCCTAGTCCACACAGCTGAG 2495
 |||||||
 Db 283 ATTACTAGTACATGAGAGAACGGCGACCTCAACACGATTCCTAGTCCACACAGCTGAG 342
 |||||||
 QY 2496 GACAGAGGACCGGAGGAGGCGCCCTTGGGAGAGGCGGACAGGCTGCGCAGAGGCCACCATCAGC 2555
 |||||||
 Db 343 GACAGAGGACCGGAGGAGGCGCCCTTGGGAGAGGCGGACAGGCTGCGCAGAGGCCACCATCAGC 402
 |||||||
 QY 2556 TACCAATGCTGCTGATGTGAGGACCCGATGCGCTCCGAGATCGGATCTGTGCGCACA 2615
 |||||||
 Db 403 TACCAATGCTGCTGATGTGAGGACCCGATGCGCTCCGAGATCGGATCTGTGCGCACA 462
 |||||||
 QY 2616 CTCAACTTTTATCATTCGAGGACCTGCGCACACGGAACCTGATAGTTGGGAAAAATTTAC 2675
 |||||||
 Db 463 CTCAACTTTTATCATTCGAGGACCTGCGCACACGGAACCTGATAGTTGGGAAAAATTTAC 522
 |||||||
 QY 2676 ATCAAAATCGCAGACTTTGGCATGAGCGGAACTCTTATGCTGGGAGCTATTTACCTGTG 2735
 |||||||
 Db 523 ATCAAAATCGCAGACTTTGGCATGAGCGGAACTCTTATGCTGGGAGCTATTTACCTGTG 582
 |||||||
 QY 2736 CAGGCGCGGCGATGCTGCCCATCCGCTGGATGAGGCTGGGATGATCTATGGGGAAG 2795
 |||||||
 Db 583 CAGGCGCGGCGATGCTGCCCATCCGCTGGATGAGGCTGGGATGATCTATGGGGAAG 642
 |||||||
 QY 2796 TTCAGAGCTGGAGAGTGAAGTGTGGGCTTTGGTGTGA--CCCTGAGGAGTGTGATGCT 2854
 |||||||
 Db 643 TTCAGAGCTGGAGAGTGAAGTGTGGGCTTTGGTGTGA--CCCTGAGGAGTGTGATGCT 702
 |||||||
 QY 2855 CTGTAGGCGCCACAGCCCTTTGGG---CAGCTACCGAGCAGCAGAGTCAATGAGAAAGCGGG 2911
 |||||||
 Db 703 CTGTAGGCGCCACAGCTTTGGGCGAGCTCAACCGAGCAGAGTCAATGAGAAAGCGGG 762
 |||||||
 QY 2912 GGAGTTCCTCCGGGACGAGGCGCGGCA--GGGTGATACCTGTCCCGGCGC--GGCTGCTGCGC 2967
 |||||||
 Db 763 GGAGTTCCTCCGGGACGAGGCGCGGCA--GGGTGATACCTGTCCCGGCGC--GGCTGCTGCGC 822
 |||||||
 QY 2968 CGCAGGCGCTA--TATGAGCTGATGCTTGTGTGTGAGCCGCGGAGTGTGACAGACGACA 3026
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 Db 823 CGCAGGCGCTA--TATGAGCTGATGCTTGTGTGTGAGCCGCGGAGTGTGACAGGAGACA 880
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 QY 3027 CCCCTTTTC 3035
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 Db 881 CCTTTTCC 889
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RESULT 8

BG912321 799 bp mRNA linear EST 05-JUN-2001
 LOCUS BG912321

DEFINITION	602806864F1 NCI CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4939239
ACCESSION	5', mRNA sequence.
VERSION	BC912321
KEYWORDS	BC912321.1 GI:14292797
SOURCE	EST.
ORGANISM	human.
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE	1 (bases 1 to 799)
JOURNAL	NH-MGC http://mgc.nci.nih.gov/.
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
	Contact: Robert Strausberg, Ph.D.
	Email: cgaabs-remail.nih.gov
	Tissue Procurement: David N. Louis, M.D.
	CDNA Library Preparation: Life Technologies, Inc.
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
	DNA Sequencing by: Incyte Genomics, Inc.
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov
	plate: LLM10875 row: 0 column: 16
	High quality sequence stop: 768.
FEATURES	Location/Qualifiers
source	1..799
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone="IMAGE:4939239"
	/clone_lib="NCI-CGAP_Brn67"
	/tissue_type="anaplastic oligodendroglioma with 1p/19q loss"
	/lab_host="DH10B (T1 phage-resistant)"
	/note="Organ: brain; Vector: pCMV-Sport6; Site: 1; NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2.3 kb. Constructed by Life Technologies. Note: this is a NCI-CGAP Library."
BASE COUNT	163 a 238 c 251 g 147 t
ORIGIN	
Query Match	17.3%; Score 684; DB 10; Length 799;
Best Local Similarity	95.7%; Pred. No. 9.4e-114;
Matches 758; Conservative	0; Mismatches 25; Indels 9; Gaps 5;
QY 2443	ACTACATGAGAAAGGGGACCTCAACAGATTCCTCAGTGTGCCACCAAGCTGAGGACAAG 2502
Db 1	ACTACATGAGAAAGGGGACCTCAACAGATTCCTCAGTGTGCCACCAAGCTGAGGACAAG 60
QY 2503	CAGCCGAGGGGGCCCTGTGGGGAGGGGCGAGGGCGGCGGAGGGGCGGAGGCGGAGTACCTACCCAA 2562
Db 61	CAGCCGAGGGGGCCCTGTGGGGAGGGGCGAGGGCGGCGGAGGGGCGGAGGCGGAGTACCTACCCAA 120
QY 2563	TGCTGCTGATGTGGCAGCCAGATCGCTCCGCGATCGCTATCTGTGGCCACACTCAACT 2622
Db 121	TGCTGCTGATGTGGCAGCCAGATCGCTCCGCGATCGCTATCTGTGGCCACACTCAACT 180
QY 2623	TTGTACATCGGGAGCTGGCCACGGGGAACTGCTAGTTGGGGAAATTTACATCAAAA 2682
Db 181	TTGTACATCGGGAGCTGGCCACGGGGAACTGCTAGTTGGGGGGAAATTTACATCAAAA 240
QY 2683	TCGCGAGACTTTGGCATGAGCCGGAACCTCTAATGCTGGGGAGATTAACGTGTGACGGCC 2742
Db 241	TCGCGAGACTTTGGCATGAGCCGGAACCTCTAATGCTGGGGAGATTAACGTGTGACGGCC 300
QY 2743	GGGAGGTCTGCCATCCGCTGTGATGCTGGGAGTGCATCTCATGTGGGAAATTCACGA 2802
Db 301	GGGAGGTCTGCCATCCGCTGTGATGCTGGGAGTGCATCTCATGTGGGAAATTCACGA 360
QY 2803	CTGCAGTGTGAGTGGGCTTTGGTGTGACCTGTGGGAGTGTGATGCTGTAGGG 2862
Db 361	CTGCAGTGTGAGTGTGGGCTTTGGTGTGACCTGTGGGAGTGTGATGCTGTAGGG 420

OY	2863	CCAGACCCCTTTGGGAGCTCACCGACGAGCAGACTCATCGAACC	CGGGGAGTTCCTTC	2922
Db	421	CCCAACCCCTTTGGGAGCTCACCGACGAGCAGACTCATCGAACC	CGGGGAGTTCCTTC	480
OY	2923	GGGACGAGGGCCGGGAGGTGTACTGTGCCGGGCCCTTGCTGC	CGCCG-C-AGGACCTATAT	2981
Db	481	GGGACGAGGGCCGGGAGGTGTACTGTGCCGGGCCCTTGCTGC	CGCCG-C-AGGACCTATAT	540
OY	2982	GAGCTGATGCTTGGTGCTGGAAGCCGGGAGCTGTAGACAGCA	CCCTTTTCCAGCTG	3041
Db	541	GAGCTGATGCTTGGTGCTGGAAGCCGGGAGCTGTAGACAGCA	CCCTTTTCCAGCTG	599
OY	3042	CATCGCTTCCTGGCAGAGATGCACCTCAACACGAGTGTAAACA	TCATCCACCTG-----	3096
Db	600	CATCGCTTCCTGGCAGAGATGCACCTCAACACGAGTGTAAACA	TCATCCACCTG-----	659
OY	3097	CCCCTCCCTCAGGAGAGTGTATCCAGGGGAGAAC-C-ACTGAC	TCTAAAA--CAAGAGACACAA	3154
Db	660	CCCCTCCCTCAGGAGAGTGTATCCAGGGGAGAAC-C-ACTGAC	TCTAAAA--CAAGAGAGACACAA	719
OY	3155	TGGCACTCTGCTCCCTCCCTCCCGACAGCCCATCACTCATATA	GAGGCACTGAGACTG	3214
Db	720	TGGCACTCTGCTCCCTCCCTCCCGACAGCCCATCACTCATATA	GAGGCACTGAGACTG	779
OY	3215	CAGGTGGGCTGG	3226	
Db	780	CAGGTGGGCTGG	791	
RESULT	9			
BE744806		715 bp	mRNA	linear EST 15-SEP-2000
LOCUS	BE744806	601575025P1 NIH_MGC_9 Homo sapiens CDNA clone IMAGE:3836046 5'		
DEFINITION	BE744806	mRNA sequence.		
ACCESSION	BE744806	GI:10158798		
VERSION	EST.			
KEYWORDS	human.			
SOURCE	Homo sapiens			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
REFERENCE	1 (bases 1 to 715)			
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.			
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL	Unpublished (1999)			
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cga@bs-femail.nih.gov Tissue Procurement: DCTD/BIP CDNA Library Preparation: Ling Hong/Rubin Laboratory DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC genome distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: Image.lnl.gov Plate: LHCMS19 row: a column: 07 High quality sequence stop: 713.			
FEATURES	location/qualifiers			
SOURCE	1..715			
	/organism="Homo sapiens"			
	/db_xref="taxon:9606"			
	/clone="IMAGE:3836046"			
	/clone_id="NIH_MGC_9"			
	/tissue_type="adenocarcinoma cell line"			
	/lab_host="DH10B (phage-resistant)"			
	/note="Organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."			
BASE COUNT	130 a	226 c	212 g	147 t
ORIGIN				

Query Match 17.2%; Score 680.4; DB 10; Length 715;
 Best Local Similarity 99.4%; Pred. No. 4.2e-113;
 Matches 714; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

QY 2682 ATCGCAGACTTGGATGAGGCGGAGCCTATGCTGGGGGAGATTACCTGTGAGAGGC 2741
 DB 1 ATCGCAGACTTGGATGAGGCGGAGCCTATGCTGGGGGAGATTACCTGTGAGAGGC 59
 QY 2742 CGGGCAGCTGCGCCATCCGCTGGATGGCTGGAGTGCATCTCTCAATGGGAGTTCAG 2801
 DB 60 CGGGCAGCTGCGCCATCCGCTGGATGGCTGGAGTGCATCTCTCAATGGGAGTTCAG 119
 QY 2802 ACTGCGAGTGTGGGCTTGGCTTGGTGTGACCTGTGGAGGTGTGTGTGTAGG 2861
 DB 120 ACTGCGAGTGTGGGCTTGGCTTGGTGTGACCTGTGGAGGTGTGTGTGTAGG 179
 QY 2862 GCCCAGCCTTGGGAGCTCACCCGAGAGTGCATGAGAGCGGGGGAGTCTTC 2921
 DB 180 GCCCAGCCTTGGGAGCTCACCCGAGAGTGCATGAGAGCGGGGGAGTCTTC 239
 QY 2922 CGGGACAGGCGCGGAGGTGTACCTGTCCCGCCCTGCTGCCGAGGCTATAT 2981
 DB 240 CGGGACAGGCGCGGAGGTGTACCTGTCCCGCCCTGCTGCCGAGGCTATAT 299
 QY 2982 GAGCTGATCTTGGTGTGTGAGCGGAGTGTGAGCAGCAGCAGCCTTTTCCAGCTG 3041
 DB 300 GAGCTGATCTTGGTGTGTGAGCGGAGTGTGAGCAGCAGCAGCCTTTTCCAGCTG 359
 QY 3042 CATCGGTTCTGCGAGAGTGCATCAACAGGCTGTGATCAACATCAGTGTGCCCC 3101
 DB 360 CATCGGTTCTGCGAGAGTGCATCAACAGGCTGTGATCAACATCAGTGTGCCCC 419
 QY 3102 CCCTCAGGAGTGTATCCAGGAGGAGGAGGAGTGCATCACTAAACAGAGAGACATGACCC 3161
 DB 420 CCCTCAGGAGGAGTGCATCAACAGGAGGAGGAGTGCATCACTAAACAGAGAGACATGACCC 478
 QY 3162 TGTGCTTCCCTCCCTCCGAGAGCCCATCACTGTATATAGAGGAGTGTGAGTGTGAG 3221
 DB 479 TGTGCTTCCCTCCCTCCGAGAGCCCATCACTGTATATAGAGGAGTGTGAGTGTGAG 538
 QY 3222 GTGGGCGCAGCAGGAGGAGTGTGCTTCCCTTCCCTTCCCTGAGACACTGTCAATGTC 3281
 DB 539 GTGGGCGCAGCAGGAGGAGTGTGCTTCCCTTCCCTTCCCTGAGACACTGTCAATGTC 598
 QY 3282 CTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3341
 DB 599 CTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 657
 QY 3342 ATCTCTCCACCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3399
 DB 658 ATCTCTCCACCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 715

RESULT 10
 BF345815 719 bp mRNA linear EST 22-NOV-2000
 LOCUS 602017891f1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153367
 DEFINITION 5', mRNA sequence.
 ACCESSION BF345815
 VERSION BF345815.1 GI:11293410
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 719)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov

Tissue Procurement: David N. Louis, M.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLM9421 row: f column: 24
 High quality sequence stop: 719.

FEATURES
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 1. 719
 Location/Qualifiers

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="IMAGE:4153367"
 /clone_lib="NCI_CGAP_Brn67"
 /tissue_type="anaplastic oligodendroglioma with 1p/19q
 loss"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site:1: NotI;
 Site:2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 2.3 kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP library."
 BASE COUNT 132 a 217 c 230 g 140 t

Query Match 17.0%; Score 672.4; DB 10; Length 719;
 Best Local Similarity 99.3%; Pred. No. 1.2e-111;
 Matches 717; Conservative 0; Mismatches 1; Indels 4; Gaps 4;

QY 2397 CTGCTGGGCGTGTGTGTGAGAGAGCAGCAGCCTTCTGATGATTAATGATCAATGAGAGC 2456
 DB 1 CTGCTGGGCGTGTGTGTGAGAGAGCAGCAGCCTTCTGATGATTAATGATCAATGAGAGC 60
 QY 2457 GGGGACCTCAACAGTCTCTAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2516
 DB 61 GGGGACCTCAACAGTCTCTAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
 QY 2517 CCGGAG 2576
 DB 121 CCGGAG 180
 QY 2577 GCAAGCCAGATGCGCTCCGAGATGCGCTATCTGCGCACACTCACTTGTATACAGGAGC 2636
 DB 181 GCAAGCCAGATGCGCTCCGAGATGCGCTATCTGCGCACACTCACTTGTATACAGGAGC 240
 QY 2637 CTGGCCAGCGGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2696
 DB 241 CTGGCCAGCGGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
 QY 2697 ATGAGCCGGAACCTCTATCTGAGGAGCTTACCGGTGTGAGAGAGAGAGAGAGAGAG 2756
 DB 301 ATGAGCCGGAACCTCTATCTGAGGAGCTTACCGGTGTGAGAGAGAGAGAGAGAGAG 360
 QY 2757 ATCCGCTGATGAGCTTGGAGTGTATCTCATGAGGAGAGAGAGAGAGAGAGAGAGAG 2816
 DB 361 ATCCGCTGATGAGCTTGGAGTGTATCTCATGAGGAGAGAGAGAGAGAGAGAGAGAG 420
 QY 2817 TGGGCGTGTGTGTGAG 2876
 DB 421 TGGGCGTGTGTGTGAG 480
 QY 2877 CAGCTCAGCAG 2936
 DB 481 CAGCTCAGCAG 539
 QY 2937 CAGGTGTACCTGTCCCGGCGCTGCTGCCGAGAGGCTATATGAGAGAGAGAGAGAGAG 2996
 DB 540 CAGGTGTACCTGTCCCGGCGCTGCTGCCGAGAGGCTATATGAGAGAGAGAGAGAGAG 599
 QY 2997 TGCTGGAG 3056
 DB 600 TGCTGGAG 658

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OY 3057 GAGATGCACTCAACA-CGGTGTGAATACACATCAAGCTCCCTCCCTCAGGAGTGA 3115
DB 659 GAGATGCACTCAACAACCGGTGTGAATACACATCCAG-TGGCCCTCCCTCAGGAGTGA 717
OY 3116 TC 3117
DB 718 TC 719

RESULT 11
LOCUS B1193181 744 bp mRNA linear EST 10-JUL-2001
DEFINITION 602947157F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:5090223 5',
mRNA sequence.
ACCESSION B1193181
VERSION B1193181.1 GI:14648201
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 744)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L1CM1852 row: b. column: 16
High quality sequence stop: 675.
Location/Qualifiers
1. 744
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/tissue_type="epitheloid carcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: pancreas; Vector: pOT7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(g). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library.]"
BASE COUNT 149 a 212 c 229 g 154 t
ORIGIN
Query Match 17 0%; Score 672; DB 10; Length 744;
Best Local Similarity 97.5%; Pred. No. 1,4e-111;
Matches 714; Conservative 0; Mismatches 15; Indels 3; Gaps 3;
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DB 2 TTTCCCTTAATGTGCGTAAGGACACCTTGTGCTGTAAGATCTTACGGC 61
OY 2297 AGATGCCACCAAGAGCCAGCTTCTCTGCTCCAGGAATGATTCTCGAAGAGGT 2356
DB 62 AGATGCCACCAAGAGCCAGCTTCTCTGCTCCAGGAATGATTCTCGAAGAGGT 121
OY 2357 GAAGATCATGTGAGGCTCAAGGACCCCAACATCATCTGGCTCTGGGCTGTGTGCA 2416
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OY 2417 GGACAGCCCTCTGCAATGATTACTGACTACATGAGAGGCGACCTCAACAGTTCT 2476
DB 182 GGAGAGCCCTCTCTGCAATGATTACTGACTACATGAGAGGCGACCTCAACAGTTCT 241
OY 2477 CAGTGGCCACAGCTGAGGAGCAAGGACCGGAGGGGCCCTTGGGAGCGGAGCTGC 2536
DB 242 CAGTGGCCACAGCTGAGGAGCAAGGACCGGAGGGGCCCTTGGGAGCGGAGCTGC 301
OY 2537 GCAGGGGCCACCATCACTACCTACCAATGCTCTGATGTGCGAGCCAGATCGCTCCG 2596
DB 302 GCAGGGGCCACCATCACTACCTACCAATGCTCTGATGTGCGAGCCAGATCGCTCCG 361
OY 2597 CATCGCTATGTGCGCACACACTCACTTGTATCATGCGGAGCTGGGCAAGGAACTGCT 2656
DB 362 CATCGCTATGTGCGCACACACTCACTTGTATCATGCGGAGCTGGGCAAGGAACTGCT 421
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OY 2897 CATGAGAAAGC-CGGGAGAGTTCTTCCGGACACAGGCGGAGAGTGTACTGTCCGGC 2955
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RESULT 12
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mRNA sequence.
ACCESSION BG696171
VERSION BG696171.1 GI:13961044
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 718)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L1AM10696 row: j column: 22
High quality sequence stop: 717.
Location/Qualifiers
1. 718
/organism="Homo sapiens"
/db_xref="taxon:9606"
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 QY 664 CCGGAGCTACCGGCTGCTTACTCCGGAGTGTCCGCTGGATGGGCTGGAAGAC 723
 DB 545 CCGGAGCTACCGGCTGCTTACTCCGGAGTGTCCGCTGGATGGGCTGGAAGAC 604
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 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
 AUTHORS NIH-MGC http://mgc.ncl.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: sgabs-remail.nih.gov
 Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: NIH Intramural Sequencing Center
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at: Image.Lnl.gov
 Plate: L1CM5 row: k column: 08
 High quality sequence start: 9
 High quality sequence stop: 702.
 Location/Qualifiers

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 /lab_host="DH10B (phage-resistant)"
 /note="organ: colon; Vector: pCM7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGACGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)"

BASE COUNT 211 a 244 c 277 g 180 t
 ORIGIN

Query Match 16.5%; Score 655.6; DB 10; Length 912;
 Best Local Similarity 95.4%; Pred. No 1.3e-108;
 Matches 740; Conservative 0; Mismatches 29; Indels 7; Gaps 6;

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 QY 3216 AGGTGGGCTGGGGCCACAGGAGGAGTATGCTCCCTCCCTCCGACAGCTGC 3275
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 DB 119 AACGGCCCATGACCTTGGGGTGGAGCATCTAGCTAGTGCAGCCCATTTTCTAT 60
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 VERSION BF944646.1 GI:12361921
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
 AUTHORS Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 662)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.R.,
 Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
 M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-Sp,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PM0642-PM0-NN1171-
181000-001-c05&f3=2000-10-18&f4=1)
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Location/Qualifiers

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/clone_lid="NN1171"
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Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT 124 a 214 c 191 g 132 t 1 others
ORIGIN

Query Match 16.5% Score 654.6; DB 10; Length 662;
Best Local Similarity 99.2% Pred. NO. 1.9e-108;
Matches 657; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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DB 181 ATATGAGCTGATGCTTGGGCTGTGAGCGGAGTGTGAGAGAGCAGCCCTTTCCCA 240
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QY 3218 GTGGGCTGGGCGCCAGCAGGAGAGTGTGCGCTTCCCTCCCTGAGACACTCTCAT 3277
DB 421 GTGGGCTGGGCGCCAGCAGGAGAGTGTGCGCTTCCCTCCCTGAGACACTCTCAT 480
QY 3278 GTCCCTTCTCTCTTCTCTCTCTAGAAAGCCCTGTGCGCCAGCCAGTGTCTGTGA 3337
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QY 3398 TAGACACTGAGATGAGCCCATTTGAGAGCAGTGGGCGCCCACTGAGACACATGATCTGG 3457
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QY 3458 AG 3459
DB 661 AG 662
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